WHAT IS CLAIMED

1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence as set forth in either SEQ ID NO: 1 or SEQ ID NO: 3;

(b) a nucleotide sequence encoding the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(c) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of (a) or (b), wherein the encoded polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4; and

(d) a nucleotide sequence complementary to any of (a)-(c).

2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide that is at least about 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 percent identical to the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 as determined using a computer program such as GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit or the Smith-Waterman algorithm;

(b) a nucleotide sequence encoding an allelic variant or splice variant of the nucleotide sequence as set forth in either SEQ ID NO: 1 or SEQ ID NO: 3, wherein the encoded polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(c) a nucleotide sequence of either SEQ ID NO: 1 or SEQ ID NO: 3; (a); or (b) encoding a polypeptide fragment of at least about 25 amino acid residues, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(d) a nucleotide sequence of either SEQ ID NO: 1 or SEQ ID NO: 3, or (a)-(c) comprising a fragment of at least about 16 nucleotides;

(e) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a)-(d), wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4; and

(f) a nucleotide sequence complementary to any of (a)-(c).

3. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(b) a nucleotide sequence encoding a polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one amino acid insertion, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(c) a nucleotide sequence encoding a polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one amino acid deletion, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(d) a nucleotide sequence encoding a polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 which has a C- and/or N- terminal truncation, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(e) a nucleotide sequence encoding a polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one modification selected from the group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(f) a nucleotide sequence of (a)-(e) comprising a fragment of at least about 16 nucleotides;

(g) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a)-(f), wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4; and

(h) a nucleotide sequence complementary to any of (a)-(e).

4. A vector comprising the nucleic acid molecule of Claims 1, 2, or 3.

5. A host cell comprising the vector of Claim 4.

6. The host cell of Claim 5 that is a eukaryotic cell.

7. The host cell of Claim 5 that is a prokaryotic cell.

8. A process of producing a CD20/IgE-receptor like polypeptide comprising culturing the host cell of Claim 5 under suitable conditions to express the polypeptide, and optionally isolating the polypeptide from the culture.

9. A polypeptide produced by the process of Claim 8.

10. The process of Claim 8, wherein the nucleic acid molecule comprises promoter DNA other than the promoter DNA for the native CD20/IgE-receptor like polypeptide operatively linked to the DNA encoding the CD20/IgE-receptor like polypeptide.

11. The isolated nucleic acid molecule according to Claim 2 wherein the percent identity is determined using a computer program selected from the group consisting of GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, and the Smith-Waterman algorithm.

12. A process for determining whether a compound inhibits CD20/IgE-receptor like polypeptide activity or production comprising exposing a cell according to Claims 5, 6, or 7 to the compound, and measuring CD20/IgE-receptor like polypeptide activity or production in said cell.

13. An isolated polypeptide comprising the amino acid sequence set forth in either SEQ ID NO: 2 or SEQ ID NO: 4.

14. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

(a) an amino acid sequence for an ortholog of either SEQ ID NO: 2 or SEQ ID NO: 4, wherein the encoded polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(b) an amino acid sequence that is at least about 70, 80, 85, 90, 95, 96, 97, 98, or 99 percent identical to the amino acid sequence of either SEQ ID NO: 2 or SEQ ID NO: 4, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 as determined using a computer program such as GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit or the Smith-Waterman algorithm;

(c) a fragment of the amino acid sequence set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 comprising at least about 25 amino acid residues, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(d) an amino acid sequence for an allelic variant or splice variant of either the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4, or at least one of (a)-(b) wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4.

15. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

(a) the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(b) the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one amino acid insertion, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(c) the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 with at least one amino acid deletion, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4;

(d) the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4 which has a C- and/or N-terminal truncation, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4; and

(e) the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4, with at least one modification selected from the group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of the polypeptide as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4.

16. An isolated polypeptide encoded by the nucleic acid molecule of Claims 1, 2, or 3.

17. The isolated polypeptide according to Claim 14 wherein the percent identity is determined using a computer program selected from the group consisting of GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, and the Smith-Waterman algorithm.

18. A polypeptide according to claim 14, 15 or 16 wherein the amino acid at position 86 of SEQ ID NO: 2 or 4 is glycine, proline, or alanine.

19. A polypeptide according to claim 14, 15 or 16 wherein the amino acid at position 95 of SEQ ID NO: 2 or 4 is leucine, valine, isoleucine, alanine, tyrosine or phenylalanine.

20. A polypeptide according to claim 14, 15 or 16 wherein the amino acid at position 103 of SEQ ID NO: 2 or 4 is isoleucine, leucine, valine, methionine, alanine, phenylalanine or norleucine.

21. A polypeptide according to claim 14, 15 or 16 wherein the amino acid at position 121 of SEQ ID NO: 2 or 4 is asparagine or glutamine.

22. A polypeptide according to claim 14, 15 or 16 wherein the amino acid at position 128 of SEQ ID NO: 2 or 4 is alanine, valine, leucine or isoleucine.

23. An antibody produced by immunizing an animal with a peptide comprising an amino acid sequence of either SEQ ID NO: 2 or SEQ ID NO: 4.

24. An antibody or fragment thereof that specifically binds the polypeptide of claims 13, 14, or 15.

25. The antibody of claim 19 that is a monoclonal antibody.

26. A hybridoma that produces a monoclonal antibody that binds to a peptide comprising an amino acid sequence of either SEQ ID NO: 2 or SEQ ID NO: 4.

27. A method of detecting or quantitating the amount of CD20/IgE-receptor like polypeptide using the anti-CD20/IgE-receptor like antibody or fragment of Claims 23 or 25.

28. A selective binding agent or fragment thereof that specifically binds at least one polypeptide wherein said polypeptide comprises the amino acid sequence selected from the group consisting of:

a) the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4; and

b) a fragment of the amino acid sequence set forth in at least one of either SEQ ID NO: 2 or SEQ ID NO: 4; and

c) a naturally occurring variant of (a) or (b).

29. The selective binding agent of Claim 28 that is an antibody or fragment thereof.

30. The selective binding agent of Claim 28 that is a humanized antibody.

31. The selective binding agent of Claim 28 that is a human antibody or fragment thereof.

32. The selective binding agent of Claim 28 that is a polyclonal antibody or fragment thereof.

33. The selective binding agent Claim 28 that is a monoclonal antibody or fragment thereof.

34. The selective binding agent of Claim 28 that is a chimeric antibody or fragment thereof.

35. The selective binding agent of Claim 28 that is a CDR-grafted antibody or fragment thereof.

36. The selective binding agent of Claim 28 that is an antiidiotypic antibody or fragment thereof.

37. The selective binding agent of Claim 28 which is a variable region fragment.

38. The variable region fragment of Claim 37 which is a Fab or a Fab' fragment.

39. A selective binding agent or fragment thereof comprising at least one complementarity determining region with specificity for a polypeptide having the amino acid sequence of either SEQ ID NO: 2 or SEQ ID NO: 4.

40. The selective binding agent of Claim 28 which is bound to a detectable label.

41. The selective binding agent of Claim 28 which antagonizes CD20/IgE-receptor like polypeptide biological activity.

42. A method for treating, preventing, or ameliorating a disease, condition, or disorder comprising administering to a patient an effective amount of a selective binding agent according to Claim 28.

43. A selective binding agent produced by immunizing an animal with a polypeptide comprising an amino acid sequence selected from the group consisting of either SEQ ID NO: 2 or SEQ ID NO: 4.

44. A hybridoma that produces a selective binding agent capable of binding a polypeptide according to Claims 1, 2, or 3.

45. A composition comprising the polypeptide of Claims 13, 14, or 15 and a pharmaceutically acceptable formulation agent.

46. The composition of Claim 45 wherein the pharmaceutically acceptable formulation agent is a carrier, adjuvant, solubilizer, stabilizer, or anti-oxidant.

47. The composition of Claim 46 wherein the polypeptide comprises the amino acid sequence as set forth in either SEQ ID NO: 2 or SEQ ID NO: 4.

48. A polypeptide comprising a derivative of the polypeptide of Claims 13, 14, or 15.

49. The polypeptide of Claim 49 which is covalently modified with a water-soluble polymer.

50. The polypeptide of Claim 49 wherein the water-soluble polymer is selected from the group consisting of polyethylene glycol, monomethoxy-polyethylene glycol, dextran, cellulose, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols, and polyvinyl alcohol.

51. A composition comprising a nucleic acid molecule of Claims 1, 2, or 3 and a pharmaceutically acceptable formulation agent.

52. A composition of Claim 51 wherein said nucleic acid molecule is contained in a viral vector.

53. A viral vector comprising a nucleic acid molecule of Claims 1, 2, or 3.

54. A fusion polypeptide comprising the polypeptide of Claims 13, 14, or 15 fused to a heterologous amino acid sequence.

55. The fusion polypeptide of Claim 54 wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

56. A method for treating, preventing or ameliorating a medical condition comprising administering to a patient the polypeptide of Claims 13, 14, or 15 or the polypeptide encoded by the nucleic acid of Claims 1, 2, or 3.

57. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of Claims 13, 14, or 15 or the polypeptide encoded by the nucleic acid molecule of Claims 1, 2, or 3 in a sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

58. A device, comprising:

(a) a membrane suitable for implantation; and

(b) cells encapsulated within said membrane, wherein said cells secrete a protein of Claims 13, 14, or 15, and wherein said membrane is permeable to said protein and impermeable to materials detrimental to said cells.

59. A device, comprising:

(a) a membrane suitable for implantation; and

(b) the CD20/IgE-receptor receptor like polypeptide of claim 13, 14 or 15 encapsulated within said membrane, wherein said membrane is permeable to the polypeptide.

60. A method of identifying a compound which binds to a polypeptide comprising:

(a) contacting the polypeptide of Claims 13, 14, or 15 with a compound; and

(b) determining the extent of binding of the polypeptide to the compound.

61. A method of modulating levels of a polypeptide in an animal comprising administering to the animal the nucleic acid molecule of Claims 1, 2, or 3.

62. A transgenic non-human mammal comprising the nucleic acid molecule of Claims 1, 2, or 3.

63. A transgenic non-human comprising a disruption of the nucleic acid molecule of claim 1, 2 or 3 wherein the expression of CD20/IgE-receptor receptor polypeptide is decreased.

64. A method of identifying antagonists of CD20/IgE-receptor receptor like polypeptide biological activity comprising:

(a) contacting a compound with an CD20/IgE-receptor receptor like polypeptide;

(b) detecting the biological activity of an CD20/IgE-receptor receptor like polypeptide in the presence of said compound; and

(c) comparing the level of CD20/IgE-receptor receptor like polypeptide biological activity in the presence and absence of said compound.

65. Then method of claim 64 wherein the compound is a small molecule, peptide, protein, carbohydrate, or antibody.

66. A method of modulating levels of a polypeptide in an animal comprising administering to the animal the nucleic acid molecule of claims 1, 2, or 3.

67. An antagonist of CD20/IgE-receptor receptor like polypeptide activity selected from the group consisting of CD20/IgE-receptor receptor like selective binding agents, small molecules, antisense oligonucleotides, and peptides or

derivatives thereof having specificity for CD20/IgE-receptor receptor like polypeptide.

68. A method of reducing cellular production of CD20/IgE-receptor receptor like polypeptide, comprising transforming or transfecting cells with a nucleic acid encoding an antagonist according to claim 67.

69. A method according to claim 68, wherein the antagonist is an antisense reagent, said reagent comprising an oligonucleotide comprising a single stranded nucleic acid sequence capable of binding to CD20/IgE-receptor receptor like mRNA.

70. A polynucleotide according to any one of claims 1 to 3 attached to a solid support.

71. An array of polynucleotides comprising at least one polynucleotide according to any one of claims 1 to 3.